

SEQUENCE LISTING



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<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921

<141> 1999-03-04

<150> 08/597,313

<151> 1996-02-06

<150> PCT/US97/02187

<151> 1997-02-06

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 30

<212> DNA

<213> Lesquerella fendleri

<400> 1

<210> 2

<211> 25

<212> DNA

<213> Lesquerella fendleri

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25

<210> 3

<211> 20

<212> DNA

<213> Lesquerella fendleri

<400> 3

ttcattaaag aggagaaatt

20

<210> 4

<211> 384

<212> PRT

<213> Lesquerella fendleri

<400> 4

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TC 1600 MAIL ROOM

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OCT 21 1999

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Glu	Thr	Glu	Ala	Leu	Lys	Arg	Gly	Pro	Cys	Glu	Lys	Pro	Pro	Phe	Thr	20	25	30	
Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	His	Cys	Phe	Lys	Arg	Ser	35	40	45	
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	Asp	Ile	Thr	Leu	Val	Ser	50	55	60	
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro	65	70	75	80
Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Val	Cys	Gln	Gly	Cys	85	90	95	
Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	Glu	Cys	Gly	His	His	Ala	100	105	110	
Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	Val	Gly	Phe	Ile	Phe	His	115	120	125	
Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	130	135	140	
His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	Asp	Glu	Val	Phe	Val	Pro	145	150	155	160
Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	Lys	Tyr	Leu	Asn	Asn	Pro	165	170	175	
Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	Phe	Ile	Leu	Gly	Trp	Pro	180	185	190	
Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	195	200	205	
Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	Lys	Asp	Arg	Glu	Arg	Leu	210	215	220	
Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Tyr	Gly	Leu	225	230	235	240
Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	Ala	Met	Ile	Cys	Val	Tyr	245	250	255	
Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	Leu	Val	Leu	Val	Thr	Phe	260	265	270	
Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Thr	Glu	Trp	275	280	285	
Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	290	295	300	

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Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
 340 345 350
 Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
 355 360 365
 Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
 370 375 380

<210> 5
 <211> 387
 <212> PRT
 <213> Ricinus communis

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 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
 20 25 30
 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
 35 40 45
 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
 50 55 60
 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
 65 70 75 80
 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
 85 90 95
 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
 100 105 110
 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
 115 120 125
 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
 130 135 140
 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
 145 150 155 160
 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
 165 170 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
 180 185 190
 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 195 200 205
 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
 210 215 220
 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
 225 230 235 240
 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
 245 250 255
 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
 260 265 270
 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
 275 280 285
 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
 290 295 300
 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
 305 310 315 320
 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
 325 330 335
 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
 340 345 350
 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
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 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
 370 375 380
 Asn Lys Tyr
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<210> 6
 <211> 383
 <212> PRT
 <213> Arabidopsis thaliana

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 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser

35					40					45									
Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Ile	Ser	Asp	Ile	Ile	Ile	Ala	Ser				
50					55					60									
Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	Ser	Leu	Leu	Pro	Gln	Pro				
65					70					75					80				
Leu	Ser	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val				
85					90					95									
Leu	Thr	Gly	Ile	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe				
100					105					110									
Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser				
115					120					125									
Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Arg	His				
130					135					140									
His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys				
145					150					155					160				
Gln	Lys	Ser	Ala	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu				
165					170					175									
Gly	Arg	Ile	Met	Met	Leu	Thr	Val	Gln	Phe	Val	Leu	Gly	Trp	Pro	Leu				
180					185					190									
Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Phe	Ala	Cys				
195					200					205									
His	Phe	Phe	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu	Gln				
210					215					220									
Ile	Tyr	Leu	Ser	Asp	Ala	Gly	Ile	Leu	Ala	Val	Cys	Phe	Gly	Leu	Tyr				
225					230					235					240				
Arg	Tyr	Ala	Ala	Ala	Gln	Gly	Met	Ala	Ser	Met	Ile	Cys	Leu	Tyr	Gly				
245					250					255									
Val	Pro	Leu	Leu	Ile	Val	Asn	Ala	Phe	Leu	Val	Leu	Ile	Thr	Tyr	Leu				
260					265					270									
Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	Tyr	Asp	Ser	Ser	Glu	Trp	Asp				
275					280					285									
Trp	Leu	Arg	Gly	Ala	Leu	Ala	Thr	Val	Asp	Arg	Asp	Tyr	Gly	Ile	Leu				
290					295					300									
Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	Thr	His	Val	Ala	His	His	Leu				
305					310					315					320				
Phe	Ser	Thr	Met	Pro	His	Tyr	Asn	Ala	Met	Glu	Ala	Thr	Lys	Ala	Ile				
325					330					335									
Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	Gln	Phe	Asp	Gly	Thr	Pro	Trp	Tyr				

340 345 350
 Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
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 Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
 370 375 380

 <210> 7
 <211> 384
 <212> PRT
 <213> Brassica napus

 <220>
 <221> PEPTIDE
 <222> (1)..(384)
 <223> encodes for hydroxylase enzyme for Brassica napus

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 20 25 30
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg
 145 150 155 160
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly
 165 170 175
 Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr
 180 185 190
 Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys

195	200	205
His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln		
210	215	220
Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu		
225	230	235 240
Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg		
	245	250 255
Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu		
	260	265 270
Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp		
	275	280 285
Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu		
	290	295 300
Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu		
305	310	315 320
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile		
	325	330 335
Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val		
	340	345 350
Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp		
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Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu Xaa		
370	375	380

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 <211> 309
 <212> PRT
 <213> Glycine max

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 20 25 30
 Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu
 35 40 45
 Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val
 50 55 60

Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr
 65 70 75 80
 Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser
 85 90 95
 Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu
 100 105 110
 Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
 115 120 125
 Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 130 135 140
 Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr
 145 150 155 160
 Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val
 165 170 175
 Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro
 180 185 190
 Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val
 195 200 205
 His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr
 210 215 220
 Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr
 225 230 235 240
 Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His
 245 250 255
 Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr
 260 265 270
 Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val
 275 280 285
 Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn
 290 295 300
 Lys Tyr Leu Arg Val
 305

<210> 9
 <211> 302
 <212> PRT
 <213> Glycine max

<400> 9
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Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val
35 40 45
Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly
50 55 60
Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr
65 70 75 80
Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu
85 90 95
Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg
100 105 110
Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu
115 120 125
Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr
130 135 140
Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu
145 150 155 160
Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
165 170 175
Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
180 185 190
Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
195 200 205
Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
210 215 220
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
225 230 235 240
Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr
245 250 255
Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala
260 265 270
Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly
275 280 285
Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val
290 295 300

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<211> 372
 <212> PRT
 <213> Zea mays

<220>
 <221> PEPTIDE
 <222> (372)
 <223> Desaturase

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 Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro
 35 40 45
 His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His
 50 55 60
 Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile
 65 70 75 80
 Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp
 85 90 95
 Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val
 100 105 110
 Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys
 115 120 125
 Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp
 130 135 140
 Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro
 145 150 155 160
 Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln
 165 170 175
 Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg
 180 185 190
 Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr
 195 200 205
 Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val
 210 215 220
 Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
 225 230 235 240
 Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
 245 250 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
 260 265 270
 Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
 275 280 285
 Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
 290 295 300
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
 305 310 315 320
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
 325 330 335
 Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
 340 345 350
 Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
 355 360 365
 Lys Lys Phe Xaa
 370

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 <211> 224
 <212> PRT
 <213> Ricinus communis

<400> 11
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 Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
 35 40 45
 Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
 50 55 60
 Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
 65 70 75 80
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
 85 90 95
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
 100 105 110
 Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
 115 120 125
 Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile

130 135 140
 Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
 145 150 155 160
 Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
 165 170 175
 Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
 180 185 190
 Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
 195 200 205
 His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
 210 215 220

<210> 12
 <211> 20
 <212> DNA
 <213> Ricinus communis

<400> 12
 gctcttttgt gcgctcattc 20

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: homologous
 regions of Ricinus communis deduced by hydroxylase
 sequence and Arabidopsis thaliana deduced desaturase
 sequence for use as oligonucleotide primer

<400> 13
 cggtaccaga aaacgccttg 20

<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220> <223> Description of Artificial Sequence: homologous
 regions of Ricinus communis deduced by hydroxylase
 sequence and Arabidopsis thaliana deduced desaturase
 sequence for use as oligonucleotide primer

<220>
 <221> primer_bind

<222> (1)..(20)

<400> 14

taywsncaym gnmgnca yca

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<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced desaturase
sequence for use as oligonucleotide primer

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21